

## SEQUENCE LISTING

<110> ITOH, Kyogo; Sumitomo Pharmaceuticals Company, Limited

<120> A Novel Tumor Antigen ART-1, and It's Tumor Antigen Peptides

<130> 661644

5 <150> Japan: 98-341253

<151> 01.12.98

<160> 21

<210> 1

<211> 414

<212> PRT

<213> Homo sapiens

<400> 1

Met Asn Leu Gln Arg Tyr Trp Gly Glu Ile Pro Ile Ser Ser Ser Gln

5

10

15

Thr Asn Arg Ser Ser Phe Asp Leu Leu Pro Arg Glu Phe Arg Leu Val

20

25

30

Glu Val His Asp Pro Pro Leu His Gln Pro Ser Ala Asn Lys Pro Lys

35

40

45

Pro Pro Thr Met Leu Asp Ile Pro Ser Glu Pro Cys Ser Leu Thr Ile

50

55

60

His Thr Ile Gln Leu Ile Gln His Asn Arg Arg Leu Arg Asn Leu Ile

65

70

75

80

Ala Thr Ala Gln Ala Gln Asn Gln Gln Gln Thr Glu Gly Val Lys Thr

25

85

90

95

Glu Glu Ser Glu Pro Leu Pro Ser Cys Pro Gly Ser Pro Pro Leu Pro

100

105

110

Asp Asp Leu Leu Pro Leu Asp Cys Lys Asn Pro Asn Ala Pro Phe Gln

115

120

125

09/857308 060101

Sub  
Pb

Ile Arg His Ser Asp Pro Glu Ser Asp Phe Tyr Arg Gly Lys Gly Glu  
 130 135 140  
 Pro Val Thr Glu Leu Ser Trp His Ser Cys Arg Gln Leu Leu Tyr Gln  
 145 150 155 160  
 Ala Val Ala Thr Ile Leu Ala His Ala Gly Phe Asp Cys Ala Asn Glu  
 165 170 175  
 Ser Val Leu Glu Thr Leu Thr Asp Val Ala His Glu Tyr Cys Leu Lys  
 180 185 190  
 Phe Thr Lys Leu Leu Arg Phe Ala Val Asp Arg Glu Ala Arg Leu Gly  
 195 200 205  
 Gln Thr Pro Phe Pro Asp Val Met Glu Gln Val Phe His Glu Val Gly  
 210 215 220  
 Ile Gly Ser Val Leu Ser Leu Gln Lys Phe Trp Gln His Arg Ile Lys  
 225 230 235 240  
 Asp Tyr His Ser Tyr Met Leu Gln Ile Ser Lys Gln Leu Ser Glu Glu  
 245 250 255  
 Tyr Glu Arg Ile Val Asn Pro Glu Lys Ala Thr Glu Asp Ala Lys Pro  
 260 265 270  
 Val Lys Ile Lys Glu Glu Pro Val Ser Asp Ile Thr Phe Pro Val Ser  
 275 280 285  
 Glu Glu Leu Glu Ala Asp Leu Ala Ser Gly Asp Gln Ser Leu Pro Met  
 290 295 300  
 Gly Val Leu Gly Ala Gln Ser Glu Arg Phe Pro Ser Asn Leu Glu Val  
 305 310 315 320  
 Glu Ala Ser Pro Gln Ala Ser Ser Ala Glu Val Asn Ala Ser Pro Leu  
 325 330 335  
 Trp Asn Leu Ala His Val Lys Met Glu Pro Gln Glu Ser Glu Glu Gly  
 340 345 350  
 Asn Val Ser Gly His Gly Val Leu Gly Ser Asp Val Phe Glu Glu Pro

Sub  
 66  
 10  
 15  
 20  
 25  
 TOT 090" 80E 25240

355                      360                      365  
 Met Ser Gly Met Ser Glu Ala Gly Ile Pro Gln Ser Pro Asp Asp Ser  
 370                      375                      380  
 Asp Ser Ser Tyr Gly Ser His Ser Thr Asp Ser Leu Met Gly Ser Ser  
 385                      390                      395                      400  
 Pro Val Phe Asn Gln Arg Cys Lys Lys Arg Met Arg Lys Ile

405

410

&lt;210&gt; 2

&lt;211&gt; 1711

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

acgcgatacct tgcctcagge ctctcgaggt ccagacagcc gccagagccg ctctgcgacg 60  
 cagcagtgaat tagtgtgta cctcctgttc tcggttcagg tccagacctc cccgtcttcc 120  
 ggctgccctg aacgtcagge gacctcagga ccctgtgatt ggcgccctgc ccggcggacc 180  
 gtgaccgagg aaacccctgg agggacttgg gcattccttg ggctccgtgc ctgttcttcg 240  
 tgctccttcc gggcaaggat ctacattat cagtctttga ccgacacaga atgcctggca 300  
 ttgataaat gtttggtgaa cttgaagaga catatggaca atg aat ctg caa aga 355

Met Asn Leu Gln Arg

5

tac tgg gga gag ata cca ata tca tca agc cag acc aac aga agt tcc 403  
 Tyr Trp Gly Glu Ile Pro Ile Ser Ser Ser Gln Thr Asn Arg Ser Ser

10

15

20

ttc gat ttg ctc cca cgg gag ttc cgt ctg gtg gaa gtc cat gac cca 451  
 Phe Asp Leu Leu Pro Arg Glu Phe Arg Leu Val Glu Val His Asp Pro

25

30

35

ccc ctg cac caa ccc tca gcc aac aag ccg aag ccc ccc act atg ctg 499  
 Pro Leu His Gln Pro Ser Ala Asn Lys Pro Lys Pro Pro Thr Met Leu

Sub  
 B6  
 10  
 15  
 20  
 25

4/12

	40	45	50	
	gac atc ccc tca gag cca tgt agt ctc acc atc cat acg att cag ttg 547			
	Asp Ile Pro Ser Glu Pro Cys Ser Leu Thr Ile His Thr Ile Gln Leu			
	55	60	65	
5	att cag cac aac cga cgt ctt cgc aac ctt att gcc aca gct cag gcc 595			
	Ile Gln His Asn Arg Arg Leu Arg Asn Leu Ile Ala Thr Ala Gln Ala			
	70	75	80	85
	cag aat cag cag cag aca gaa ggt gta aaa act gaa gag agt gaa cct 643			
	Gln Asn Gln Gln Gln Thr Glu Gly Val Lys Thr Glu Glu Ser Glu Pro			
	90	95	100	
10	ctt ccc tgc tgc cct ggg tca cct cct ctc cct gat gac ctc ctg cct 691			
	Leu Pro Ser Cys Pro Gly Ser Pro Pro Leu Pro Asp Asp Leu Leu Pro			
	105	110	115	
	tta gat tgt aag aat ccc aat gca cca ttc cag atc cgg cac agt gac 739			
15	Leu Asp Cys Lys Asn Pro Asn Ala Pro Phe Gln Ile Arg His Ser Asp			
	120	125	130	
	cca gag agt gac ttt tat cgt ggg aaa ggg gaa cct gtg act gaa ctc 787			
	Pro Glu Ser Asp Phe Tyr Arg Gly Lys Gly Glu Pro Val Thr Glu Leu			
	135	140	145	
20	agc tgg cac tcc tgt cgg cag ctc ctc tac cag gca gtg gcc aca atc 835			
	Ser Trp His Ser Cys Arg Gln Leu Leu Tyr Gln Ala Val Ala Thr Ile			
	150	155	160	165
	ctg gcc cac gcg ggc ttt gac tgt gct aat gag agt gtc ctg gag acc 883			
	Leu Ala His Ala Gly Phe Asp Cys Ala Asn Glu Ser Val Leu Glu Thr			
25	170	175	180	
	cta act gat gtg gca cat gag tat tgc ctt aag ttt acc aag ttg ctg 931			
	Leu Thr Asp Val Ala His Glu Tyr Cys Leu Lys Phe Thr Lys Leu Leu			
	185	190	195	
	cgt ttt gct gtg gac cgg gag gcc cgg ctg gga cag act cct ttt cct 979			

Sub  
B6

101090" 90E25850

Arg Phe Ala Val Asp Arg Glu Ala Arg Leu Gly Gln Thr Pro Phe Pro  
 200 205 210  
 gat gtg atg gag cag gta ttc cat gaa gtg ggt att ggc agt gtg ctc 1027  
 Asp Val Met Glu Gln Val Phe His Glu Val Gly Ile Gly Ser Val Leu  
 5 215 220 225  
 tcc ctc cag aag ttc tgg cag cac cgc atc aag gac tat cac agt tac 1075  
 Ser Leu Gln Lys Phe Trp Gln His Arg Ile Lys Asp Tyr His Ser Tyr  
 230 235 240 245  
 atg cta cag att agt aag caa ctc tct gaa gaa tat gaa agg att gtc 1123  
 Met Leu Gln Ile Ser Lys Gln Leu Ser Glu Glu Tyr Glu Arg Ile Val  
 250 255 260  
 aat cct gag aag gcc aca gag gac gct aaa cct gtg aag atc aag gag 1171  
 Asn Pro Glu Lys Ala Thr Glu Asp Ala Lys Pro Val Lys Ile Lys Glu  
 265 270 275  
 gaa cct gtg agc gac atc act ttt cct gtc agt gag gag ctg gag gct 1219  
 Glu Pro Val Ser Asp Ile Thr Phe Pro Val Ser Glu Glu Leu Glu Ala  
 280 285 290  
 gac ctt gct tct gga gac cag tca ctg cct atg gga gtg ctt ggg gct 1267  
 Asp Leu Ala Ser Gly Asp Gln Ser Leu Pro Met Gly Val Leu Gly Ala  
 20 295 300 305  
 cag agc gaa cgc ttc cca tct aac ctg gag gtt gaa gct tca cca cag 1315  
 Gln Ser Glu Arg Phe Pro Ser Asn Leu Glu Val Glu Ala Ser Pro Gln  
 310 315 320 325  
 gct tca agt gca gag gta aat gct tct cct ctt tgg aat ctg gcc cat 1363  
 Ala Ser Ser Ala Glu Val Asn Ala Ser Pro Leu Trp Asn Leu Ala His  
 25 330 335 340  
 gtg aaa atg gag cct caa gaa agt gaa gaa ggc aat gtc tct ggg cat 1411  
 Val Lys Met Glu Pro Gln Glu Ser Glu Glu Gly Asn Val Ser Gly His  
 345 350 355

Sub  
 Be  
 10  
 15  
 20  
 25

ggt gtg ctg ggc agt gat gtc ttc gag gag cct atg tca ggc atg agt 1459  
 Gly Val Leu Gly Ser Asp Val Phe Glu Glu Pro Met Ser Gly Met Ser

360

365

370

gaa gct ggg att cct cag agc cct gat gac tca gat agc agc tat ggt 1507  
 5 Glu Ala Gly Ile Pro Gln Ser Pro Asp Asp Ser Asp Ser Ser Tyr Gly

375

380

385

tcc cac tcc act gac agc ctc atg ggg tcc tcc cct gtt ttc aac cag 1555  
 Ser His Ser Thr Asp Ser Leu Met Gly Ser Ser Pro Val Phe Asn Gln

390

395

400

405

cgc tgc aag aag agg atg agg aaa ata taaaaggaaa agagggagat 1602  
 Arg Cys Lys Lys Arg Met Arg Lys Ile

410

gttttgtcca gacctactag acccaacaga aaagggtttt gtattagaat ctgtttcctt 1662  
 aaaaattgat ttgactcctg ttcttaaaaa aaaaaaaaaa aaaaaaaaaa 1711

&lt;210&gt; 3

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

Gly Phe Asp Cys Ala Asn Glu Ser Val Leu

5

10

&lt;210&gt; 4

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

Glu Tyr Cys Leu Lys Phe Thr Lys Leu

Sub  
 Pl

00857308.0601.01  
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<210> 5

<211> 8

&lt;212&gt; PRT

<213> Homo sapiens

<400> 5

Leu Tyr Gln Ala Val Ala Thr Ile

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<210> 6

&lt;211&gt; 9

&lt;212&gt; PRT

<213> Homo sapiens

<400> 6

Ser Phe Asp Leu Leu Pro Arg/Glu Phe

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<210> 7

&lt;211&gt; 11

&lt;212&gt; PRT

<213> Homo sapiens

<400> 7

Ser Phe Asp/Leu Leu Pro Arg Glu Phe Arg Leu

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5

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 $\langle 210 \rangle / 8$ 

~~<211>~~ 9

~~<212>~~ PRT

8/12

<213> Homo sapiens

<400> 8

Leu Tyr Gln Ala Val Ala Thr Ile Leu

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<210> 9

<211> 10

<212> PRT

<213> Homo sapiens

<400> 9

Glu Tyr Cys Leu Lys Phe Thr Lys Leu Leu

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<210> 10

<211> 10

<212> PRT

<213> Homo sapiens

<400> 10

Arg Phe Ala Val Asp Met Glu Gln Val Phe

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5

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<210> 11

<211> 10

<212> PRT

25

<213> Homo sapiens

<400> 11

Pro Phe Pro Asp Val Met Glu Gln Val Phe

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Sub  
B6

00057300 060101  
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<210> 12

&lt;211&gt; 11

&lt;212&gt; PRT

<213> Homo sapiens

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Val Phe His Glu Val Gly Ile Gly Ser Val Leu

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&lt;210&gt; 13

&lt;211&gt; 9

&lt;212&gt; PRT

<213> Homo sapiens

&lt;400&gt; 13

Asp Tyr His Ser Tyr Met Leu Gln Ile

5

&lt;210&gt; 14

<211> 10

&lt;212&gt; PRT

20            <213> Homo sapiens

<400> 14

Ser Tyr Met/Leu Gln Ile Ser Lys Gln Leu

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10

25       $\langle 210 \rangle / 15$

~~211~~ 10

~~<212>~~ PRT

~~213~~ Homo sapiens

/ <400> 15

10 15

10/12

Ser Tyr Gly Ser His Ser Thr Asp Ser Leu

5

10

<210> 16

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<211> 8

<212> PRT

<213> Homo sapiens

<400> 16

Arg Tyr Trp Gly Glu Ile Pro Ile

5

<210> 17

<211> 8

<212> PRT

<213> Homo sapiens

<400> 17

Lys Phe Thr Lys Leu Leu Arg Phe

5

20

<210> 18

<211> 8

<212> PRT

<213> Homo sapiens

<400> 18

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Thr Phe Pro Val Ser Glu Glu Leu

5

<210> 19

<211> 10

101090" 80E25868

Sub  
B6  
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060101

25

12/12

<210> 21

<211> 8

<212> PRT

<213> Artificial Sequence

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<221> VARIANT

<222> 2

<223> Xaa is Phe, Tyr, Met or Trp.

<220>

<221> VARIANT

<222> 8

<223> Xaa is Phe, Leu, Ile, Trp or Met.

<400> 21

Leu Xaa Gln Ala Val Ala Thr Xaa

5

5

10

15

TOF090" 80E25868

Sub  
B6